



SEQUENCE LISTING

<110> Choe, Sunghwa
Feldmann, Kenneth A

<120> Dwf7 MUTANTS

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<140> 09/775,879

<141> 2001-02-02

<150> 60/179,901

<151> 2000-02-02

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<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer S5D_1F

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<210> 4

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 <223> Description of Artificial Sequence: Primer S5D_1R

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 <400> 5
 gatgcacaga gagcttcatg ac 22

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 <210> 9

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<223> Description of Artificial Sequence: Primer D7-5-1

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32

<210> 10

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<223> Description of Artificial Sequence: Primer D7-5-2

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aagtatagta gggttccggc gaggta

26

<210> 11

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<223> Description of Artificial Sequence: Primer D7-5-3

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<210> 12

<211> 32

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<223> Description of Artificial Sequence: Primer D7-3-1

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32

<210> 13

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<223> Description of Artificial Sequence: Primer D7-3-2

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 <213> Artificial Sequence

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<210> 15
 <211> 364
 <212> PRT
 <213> delta-7 sterol C-5 desaturase (Candida glabrata)

<400> 15
 Met Asp Leu Val Leu Glu Thr Leu Asp His Tyr Ile Phe Asp Asp Val
 1 5 10 15
 Tyr Ala Lys Ile Ala Pro Val Glu Leu Gln Arg Gly Ile Asp Asp Ser
 20 25 30
 Leu Val Asn Ala Leu Ser Leu Asn Lys Ile Val Ser Asn Ser Thr Leu
 35 40 45
 Leu His Glu Thr Leu Ser Ile Thr Asn Ser Leu Lys Arg Val Asn Lys
 50 55 60
 Asp Val Tyr Gly Leu Thr Pro Phe Leu Phe Asp Phe Thr Glu Lys Thr
 65 70 75 80
 Tyr Ala Ser Leu Leu Pro Arg Asn Asn Leu Ile Arg Glu Phe Phe Ser
 85 90 95
 Leu Trp Ala Val Val Thr Val Phe Gly Leu Leu Leu Tyr Leu Ile Thr
 100 105 110
 Ala Ser Leu Ser Tyr Val Phe Val Phe Asp Arg Thr Ile Phe Asn His
 115 120 125
 Pro Lys Tyr Leu Lys Asn Gln Met Tyr Leu Glu Ile Lys Leu Ala Val
 130 135 140
 Ser Ala Ile Pro Thr Met Ser Leu Leu Thr Val Pro Trp Phe Met Leu
 145 150 155 160
 Glu Leu Asn Gly Tyr Ser Lys Leu Tyr Tyr Asp Val Asp Trp Glu His
 165 170 175
 His Gly Leu Arg Lys Leu Leu Ile Glu Tyr Ala Thr Phe Ile Phe Phe
 180 185 190
 Thr Asp Cys Gly Ile Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg

<210> 17
 <211> 329
 <212> PRT
 <213> delta-7 sterol C-5 desaturase (Schizosaccharomyces pombe)

<400> 17
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 Thr Ala Val Asn Ser Thr Thr Leu Gly Leu Ala Glu Lys Val Asn Phe
 35 40 45
 Ala Ile Thr Ser Gly Leu Leu Asp Arg Asn Asn Val Trp Arg Gln Phe
 50 55 60
 Thr Ser Leu Phe Leu Ile Thr Trp Ile Met Gly Thr Leu Ser Tyr Phe
 65 70 75 80
 Leu Ser Ala Ser Phe Ala Tyr Tyr Val Tyr Phe Asp Arg Glu Glu Ala
 85 90 95
 Arg Arg His Pro Lys Phe Leu Lys Asn Gln Glu His Leu Glu Leu Met
 100 105 110
 Val Ala Leu Lys Asn Leu Pro Gly Met Ala Ile Leu Thr Ala Pro Trp
 115 120 125
 Phe Leu Ala Glu Ile Arg Gly Tyr Gly Tyr Val Tyr Asp Lys Leu Asp
 130 135 140
 Glu Tyr Gly Tyr Phe Tyr Leu Phe Phe Ser Ile Ala Leu Phe Leu Leu
 145 150 155 160
 Phe Ser Asp Phe Leu Ile Tyr Trp Ile His Arg Ala Leu His His Arg
 165 170 175
 Trp Leu Tyr Ala Pro Leu His Lys Leu His His Lys Trp Ile Val Pro
 180 185 190
 Thr Pro Tyr Ser Ser His Ala Phe His Tyr Leu Asp Gly Tyr Ser Gln
 195 200 205
 Ser Leu Pro Tyr His Met Phe Pro Phe Phe Phe Pro Leu Asn Lys Tyr
 210 215 220
 Val Tyr Leu Leu Leu Phe Gly Ser Val Asn Tyr Trp Thr Val Leu Ile
 225 230 235 240
 His Asp Gly Lys Tyr Phe Ser Asn Asn Ala Val Val Asn Gly Ala Ala
 245 250 255

His His Ala Ala His His Met Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe
260 265 270

Phe Thr Leu Phe Asp Arg Leu Cys Ser Ser Tyr Arg Gln Pro Asp Gln
275 280 285

Glu Leu Phe Asp Ala Glu Leu Arg Asn Glu Lys Leu Gln Glu Gln Arg
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Arg Thr Tyr Ala Ser Lys Lys Asp Asn
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<210> 18
<211> 281
<212> PRT
<213> DWF7/STE1 (Arabidopsis)

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20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu
275 280

<210> 19

<211> 291

<212> PRT

<213> delta-7 sterol C-5 desaturase concensus

<400> 19

Met Asp Leu Val Leu Glu Ala Asp His Tyr Val Phe Asp Asp Tyr Ala
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Lys Ile Pro Leu Ala Ile Asp Ser Leu Leu Asn Val Ser Asn Ser Thr
20 25 30

Leu Glu Thr Leu Asn Lys Val Asn Tyr Gly Pro Phe Leu Phe Asp Phe
35 40 45

Thr Glu Thr Ser Phe Ser Leu Leu Pro Arg Asn Asn Leu Trp Arg Glu
50 55 60

Phe Leu Ser Leu Trp Leu Ile Val Thr Ile Phe Gly Leu Leu Tyr Ile
65 70 75 80

Ala Ser Leu Ser Tyr Phe Phe Asp Ile Phe Asn His Pro Lys Tyr Leu
85 90 95

Lys Asn Gln Met Leu Glu Ile Lys Ala Val Ala Ile Pro Trp Met Ser
100 105 110

Leu Leu Thr Val Pro Trp Phe Met Glu Leu Gly Tyr Ser Lys Leu Tyr
115 120 125

Lys Ile Asp Glu His Gly Arg Lys Leu Phe Ile Glu Ala Thr Phe Phe
130 135 140

Phe Thr Asp Gly Ile Tyr Ala His Arg Trp Leu His Trp Pro Tyr Lys
145 150 155 160

Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro Phe Ala
165 170 175

Ser His Ala Phe His Pro Val Asp Gly Tyr Leu Gln Ser Leu Tyr His
180 185 190

Ile Tyr Pro Leu Leu Pro Leu His Lys Ser Tyr Leu Leu Phe Thr Phe
195 200 205

Val Asn Phe Trp Thr Val Met Ile His Asp Gly Gln Ser Asn Asn Pro
210 215 220

Val Val Asn Gly Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr
225 230 235 240

Asn Tyr Gly Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr
245 250 255

Arg Arg Pro Asp Ser Leu Phe Asp Pro Lys Leu Arg Asp Lys Lys Glu
260 265 270

Gln Arg Glu Thr Tyr Ile Glu Val Glu Gly Asp Asp Arg Tyr Asp
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Lys Lys Asn
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<210> 20

<211> 1889

<212> DNA

<213> Genomic dwf7 (Arabidopsis)

<400> 20

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tctcggtgga tctccgattc acatggcggc ggataatgct tatctgatgc agtttggtga 180
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<210> 21
 <211> 281
 <212> PRT
 <213> DWF7

<400> 21

Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser
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Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
 20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
 35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
 50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
 65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
 85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
 100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
 115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
 130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
 145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
 165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu
275 280

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<211> 2925
<212> DNA
<213> Genomic HDF7

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 <212> PRT
 <213> HDF7

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Trp Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu
    35              40              45

Ala Gly Asn Ile Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr
    50              55              60

Ile Tyr Tyr Leu Lys Leu Asn Val Tyr Val Pro Lys Glu Ser Ile Pro
    65              70              75              80

Thr Arg Lys Ala Met Leu Leu Gln Ile Tyr Val Ala Met Lys Ala Met
          85              90              95

Pro Trp Tyr Thr Leu Leu Pro Ala Val Ser Glu Tyr Met Ile Glu His
    100              105              110

Gly Trp Thr Lys Cys Tyr Ser Thr Leu Asp His Phe Asn Trp Phe Leu
    115              120              125

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Cys Phe Leu Tyr Ile Ala Leu Tyr Leu Val Leu Val Glu Phe Met Ile
130 135 140

Tyr Trp Val His Lys Glu Leu His Asp Ile Lys Phe Leu Tyr Lys His
145 150 155 160

Leu His Ala Thr His His Met Tyr Asn Lys Gln Asn Thr Leu Ser Pro
165 170 175

Phe Ala Gly Leu Ala Phe His Pro Leu Asp Gly Ile Leu Gln Ala Ile
180 185 190

Pro His Val Ile Ala Leu Phe Ile Val Pro Ile His Leu Ile Thr His
195 200 205

Leu Ser Leu Leu Phe Leu Glu Gly Ile Trp Thr Ala Ser Ile His Asp
210 215 220

Cys Ile His Gly Asn Ile Trp Pro Ile Met Gly Ala Gly Tyr His Thr
225 230 235 240

Ile His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp
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Met Asp Trp Met Phe Gly Ser Leu Met Val Pro Leu Ala Glu Lys Asp
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Ser Phe Lys Glu Lys Glu Lys
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<213> dwf7-2

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20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
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Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp
50 55 60

<210> 25
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<212> PRT
<213> dwf7-1

<400> 25

Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser
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Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp
225 230